



1

SEQUENCE LISTING

<110> TURCK, JUTTA
ARCHER, JOHN

<120> CONTROL OF GENE EXPRESSION IN EUKARYOTES

<130> 13101/48202

<140> 10/732,859

<141> 2003-12-09

<150> 09/469,211

<151> 1999-12-22

<150> 9828660.2

<151> 1998-12-24

<160> 19

<170> PatentIn version 3.3

<210> 1

<211> 7599

<212> DNA

<213> Rhodococcus sp.

<220>

<221> CDS

<222> (295)..(1035)

<220>

<221> CDS

<222> (1261)..(2805)

<220>

<221> CDS

<222> (2807)..(4720)

<220>

<221> CDS

<222> (5721)..(6665)

<400> 1

gaattccatg ttcttctcct tgcattgtggc ccgcgttgcc gagggcactg ctcggcctgt 60

cgcccgacaga gggcgcatgt ccgggtgcct ggatatggcg cgtacggcgt gccctccggc 120

gttaaccccg aggttggcca cgatgccccg gccatcaggt ctggaatgct agcggtccag 180

acgaaggtaa cccacagtga ctcacaccac aagtactaga atgcaagctg ttgcggtgag 240

cgccgcggca taagggggag ccatgtccgg gacgccgacg gaaagcctga ctcg atg 297
Met

1

acc	acc	acc	gac	acc	ggc	ccc	aag	ccg	ggc	agt	gag	gcc	gcc	gcc	ctg	345
Thr	Thr	Thr	Asp	Thr	Gly	Pro	Lys	Pro	Gly	Ser	Glu	Ala	Ala	Ala	Leu	
		5						10					15			
ctc	gcc	aat	gtc	cgc	acc	tcg	ggg	gcg	cgg	ctg	tcc	tcc	gcg	ttg	tac	393
Leu	Ala	Asn	Val	Arg	Thr	Ser	Gly	Ala	Arg	Leu	Ser	Ser	Ala	Leu	Tyr	
		20					25					30				
gac	att	ctg	aag	aac	cgg	ctg	ctc	gaa	ggg	cgc	tat	gcg	gca	ggc	gag	441
Asp	Ile	Leu	Lys	Asn	Arg	Leu	Leu	Glu	Gly	Arg	Tyr	Ala	Ala	Gly	Glu	
	35					40					45					
aag	atc	gtc	gtc	gag	tcg	atc	cgg	caa	gag	ttc	ggg	gtg	agc	aag	cag	489
Lys	Ile	Val	Val	Glu	Ser	Ile	Arg	Gln	Glu	Phe	Gly	Val	Ser	Lys	Gln	
50					55					60					65	
ccc	gtc	atg	gac	gct	ctg	cgc	cgc	ctg	tcc	agc	gac	aag	ctg	gtc	cac	537
Pro	Val	Met	Asp	Ala	Leu	Arg	Arg	Leu	Ser	Ser	Asp	Lys	Leu	Val	His	
				70					75					80		
atc	gtt	ccc	cag	gtc	ggc	tgc	gag	gtc	gtc	tcc	tac	gcc	ccg	cgc	gaa	585
Ile	Val	Pro	Gln	Val	Gly	Cys	Glu	Val	Val	Ser	Tyr	Ala	Pro	Arg	Glu	
			85				90						95			
gtg	gaa	gac	ttc	tac	acc	ctg	ttc	ggc	ggc	ttc	gaa	ggg	acc	atc	gcc	633
Val	Glu	Asp	Phe	Tyr	Thr	Leu	Phe	Gly	Gly	Phe	Glu	Gly	Thr	Ile	Ala	
		100					105					110				
gcg	gta	gcg	gcc	tcc	cgg	cgg	acc	gag	gcc	cag	ttg	ctg	gag	ctg	gac	681
Ala	Val	Ala	Ala	Ser	Arg	Arg	Thr	Glu	Ala	Gln	Leu	Leu	Glu	Leu	Asp	
	115					120					125					
ctg	atc	tcg	gcg	cgg	gtc	gac	gcc	ctg	atc	acc	tcc	cac	gac	ccg	gtg	729
Leu	Ile	Ser	Ala	Arg	Val	Asp	Ala	Leu	Ile	Thr	Ser	His	Asp	Pro	Val	
130					135					140					145	
gtc	cgc	gcc	cgc	ggg	tac	cgc	gtg	cac	aac	cgg	gag	ttc	cat	gcg	gcc	777
Val	Arg	Ala	Arg	Gly	Tyr	Arg	Val	His	Asn	Arg	Glu	Phe	His	Ala	Ala	
				150					155					160		
atc	cac	gcg	atg	gcg	cac	tcg	cgg	atc	atg	gag	gag	acc	agc	cag	cga	825
Ile	His	Ala	Met	Ala	His	Ser	Arg	Ile	Met	Glu	Glu	Thr	Ser	Gln	Arg	
			165					170					175			
atg	tgg	gat	ctg	tcg	gac	ttc	ttg	atc	aac	acc	acc	ggc	atc	acc	aac	873
Met	Trp	Asp	Leu	Ser	Asp	Phe	Leu	Ile	Asn	Thr	Thr	Gly	Ile	Thr	Asn	
		180					185					190				
ccg	ctc	tcg	agc	gca	ctg	ccc	gac	cgg	cag	cat	gac	cac	cac	gaa	atc	921
Pro	Leu	Ser	Ser	Ala	Leu	Pro	Asp	Arg	Gln	His	Asp	His	His	Glu	Ile	
		195				200					205					
acc	gag	gcc	atc	cgc	aac	cgt	gac	gca	gct	gcc	gcc	cgc	gag	gcc	atg	969
Thr	Glu	Ala	Ile	Arg	Asn	Arg	Asp	Ala	Ala	Ala	Ala	Arg	Glu	Ala	Met	
210					215					220					225	

gaa cgc cac atc gtc ggc acc atc gca gta atc cgc gac gaa tcc aac	1017
Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser Asn	
230 235 240	
gcc cag ctg ccg agc tag accccgatac ccggggccatc gaccggctcc	1065
Ala Gln Leu Pro Ser	
245	
gctatcgcgc cacctacgcc gagggggggac tctcggccgt agcgctgcag acgatccacc	1125
ggcaccctcc acgctgaccc ctgtctcgcc ctagagggcc ggcgcgccgt cgatcacctt	1185
taccctcatc cagagacttg cgtcacctc tatgcccagag tagcgtctga actagacgtc	1245
tagcattcta gttga gtg ctc cct ctc gaa gat tct cca gag aac ccc tct	1296
Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser	
250 255	
cga aca tcc cca gaa gaa agg agc ggc cat gac gac cgc ttc gca cgc	1344
Arg Thr Ser Pro Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg	
260 265 270	
atc gtc ctt cgg ggc acg agc cca ctt ccg ccc aca gat cgg gga agc	1392
Ile Val Leu Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser	
275 280 285 290	
ccg acc gtg agc acc aca cct acc tcc ccg acg aag acc tca ccg ctg	1440
Pro Thr Val Ser Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu	
295 300 305	
cgg gta gcg atg gcc agc ttc atc ggt acc acc gtc gag tac tac gac	1488
Arg Val Ala Met Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp	
310 315 320	
ttc ttc atc tac ggc acc gcg gcc gcg ctg gta ttc cct gag ttg ttc	1536
Phe Phe Ile Tyr Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe	
325 330 335	
ttc ccg gat gtc tcg tcc gcg atc gga atc ctg ttg tcg ttc gcg acc	1584
Phe Pro Asp Val Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr	
340 345 350	
ttc agc gtt ggg ttc ctc gcc cgc ccg ctg ggt ggc ata gtg ttc ggg	1632
Phe Ser Val Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly	
355 360 365 370	
cac ttc ggt gac cgg gtc ggc cgc aag cag atg ctg gtg atc tcc ctg	1680
His Phe Gly Asp Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu	
375 380 385	
gtc gga atg ggc tcg gcc acc gta ctg atg gga ttg ttg ccc ggt tac	1728
Val Gly Met Gly Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr	
390 395 400	
gcc caa atc ggg atc gcc gcc ccc atc ctg ctg acc ctg ctg cgc ctg	1776
Ala Gln Ile Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu	
405 410 415	

gtg	cag	ggc	ttt	gcc	gtc	ggc	ggc	gag	tgg	ggc	gga	gcc	acc	ctg	atg	1824
Val	Gln	Gly	Phe	Ala	Val	Gly	Gly	Glu	Trp	Gly	Gly	Ala	Thr	Leu	Met	
420						425				430						
gcc	gtc	gag	cac	gcc	ccc	acc	gcg	aag	aag	ggc	ttt	ttc	gga	tcc	ttc	1872
Ala	Val	Glu	His	Ala	Pro	Thr	Ala	Lys	Lys	Gly	Phe	Phe	Gly	Ser	Phe	
435					440					445					450	
tcc	cag	atg	ggg	gca	ccc	gcc	ggg	acc	agc	gtc	gca	acc	ctg	gcg	ttc	1920
Ser	Gln	Met	Gly	Ala	Pro	Ala	Gly	Thr	Ser	Val	Ala	Thr	Leu	Ala	Phe	
				455					460					465		
ttc	gcg	gtc	tcc	caa	ttg	ccc	gac	gag	cag	ttc	ctg	agt	tgg	ggc	tgg	1968
Phe	Ala	Val	Ser	Gln	Leu	Pro	Asp	Glu	Gln	Phe	Leu	Ser	Trp	Gly	Trp	
			470					475					480			
cga	ctg	ccg	ttc	ctg	ttc	agc	gcg	gtg	ctg	atc	gtg	atc	ggg	ctg	ttc	2016
Arg	Leu	Pro	Phe	Leu	Phe	Ser	Ala	Val	Leu	Ile	Val	Ile	Gly	Leu	Phe	
	485						490					495				
att	cgc	ctg	tcc	ctg	gcc	gaa	agc	ccc	gac	ttc	gcc	gag	gtg	aag	gca	2064
Ile	Arg	Leu	Ser	Leu	Ala	Glu	Ser	Pro	Asp	Phe	Ala	Glu	Val	Lys	Ala	
500						505					510					
cag	agc	gcc	gtg	gtg	cga	atg	ccg	atc	gcc	gaa	gcg	ttc	cgc	aag	cac	2112
Gln	Ser	Ala	Val	Val	Arg	Met	Pro	Ile	Ala	Glu	Ala	Phe	Arg	Lys	His	
515					520					525					530	
tgg	aag	gaa	att	ctc	ctc	atc	gcg	ggc	acc	tac	ctg	tcc	caa	gga	gtg	2160
Trp	Lys	Glu	Ile	Leu	Leu	Ile	Ala	Gly	Thr	Tyr	Leu	Ser	Gln	Gly	Val	
				535					540					545		
ttc	gcc	tat	atc	tgc	atg	gcc	tac	ctc	gtc	tcc	tac	ggc	acc	acc	gtc	2208
Phe	Ala	Tyr	Ile	Cys	Met	Ala	Tyr	Leu	Val	Ser	Tyr	Gly	Thr	Thr	Val	
			550					555					560			
gcg	ggg	atc	agc	cgc	acc	ttc	gcc	ctg	gcc	gga	gta	ttc	gtc	gcc	ggc	2256
Ala	Gly	Ile	Ser	Arg	Thr	Phe	Ala	Leu	Ala	Gly	Val	Phe	Val	Ala	Gly	
	565						570					575				
atc	gtc	gcc	gtc	ctc	ctc	tac	ctc	gtg	ttc	ggc	gct	ctg	tcc	gac	act	2304
Ile	Val	Ala	Val	Leu	Leu	Tyr	Leu	Val	Phe	Gly	Ala	Leu	Ser	Asp	Thr	
	580					585					590					
ttc	ggc	cgc	aag	acc	atg	tac	ctg	ctc	ggc	gcc	gcc	gcg	atg	ggc	gtg	2352
Phe	Gly	Arg	Lys	Thr	Met	Tyr	Leu	Leu	Gly	Ala	Ala	Ala	Met	Gly	Val	
595					600				605						610	
gtg	atc	gcc	ccc	gcc	ttc	gca	ctg	atc	aac	acc	ggc	aac	ccg	tgg	ctg	2400
Val	Ile	Ala	Pro	Ala	Phe	Ala	Leu	Ile	Asn	Thr	Gly	Asn	Pro	Trp	Leu	
				615					620					625		
ttc	atg	gcc	gcg	cag	gtg	ctg	gtc	ttc	gga	att	gca	atg	gcc	ccc	gcc	2448
Phe	Met	Ala	Ala	Gln	Val	Leu	Val	Phe	Gly	Ile	Ala	Met	Ala	Pro	Ala	
			630					635					640			

gcc ggc gtg aca ggc tcc ctg ttc acg atg gtc ttc gac gcg gac gtg Ala Gly Val Thr Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val 645 650 655	2496
cgc tac agc ggt gtc tct atc ggc tac acc atc tcc cag gtc gcc ggc Arg Tyr Ser Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly 660 665 670	2544
tcc gcg ttc gcc ccg acg atc gcg acc gcc ttg tac gcc tcc acc aac Ser Ala Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn 675 680 685 690	2592
acc agc aac tcg atc gtg acc tac ctg ctg atc gtc tcg gcc atc tcg Thr Ser Asn Ser Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser 695 700 705	2640
atc gtc tcg gtg atc ctg ctg ccc ggc ggc tgg ggg cgc aag ggc gct Ile Val Ser Val Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala 710 715 720	2688
gcg agc cag ctc act cgc gac cag gcc acc tcc aca ccg aaa atg cct Ala Ser Gln Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro 725 730 735	2736
gac acc gaa aca ttt tcg act cgg aca gtt ccg gac acc gca gca tcc Asp Thr Glu Thr Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser 740 745 750	2784
ctg cgc gtc ctc gac aag tga a gtg atg aca gac atg agt gac cac gac Leu Arg Val Leu Asp Lys Val Met Thr Asp Met Ser Asp His Asp 755 760 765	2833
cgc acc tcc tac gac acc gac gtc gtg atc gtc ggc ctc ggc ccc gcc Arg Thr Ser Tyr Asp Thr Asp Val Val Ile Val Gly Leu Gly Pro Ala 770 775 780 785	2881
ggt ggc aca gcg gcg ctt gcc ctg gcc agc tac ggc atc cgc gtt cac Gly Gly Thr Ala Ala Leu Ala Leu Ala Ser Tyr Gly Ile Arg Val His 790 795 800	2929
gcc gtc tcg atg ttc ccc tgg gtg gcg aac tcg ccg cgc gcg cac atc Ala Val Ser Met Phe Pro Trp Val Ala Asn Ser Pro Arg Ala His Ile 805 810 815	2977
acc aac cag cgc gcc gtc gaa gtg ctg cgt gac ctg ggc gtc gaa gac Thr Asn Gln Arg Ala Val Glu Val Leu Arg Asp Leu Gly Val Glu Asp 820 825 830	3025
gag gcg cgc aac tac gcc acc ccg tgg gac cag atg ggc gac acg ctg Glu Ala Arg Asn Tyr Ala Thr Pro Trp Asp Gln Met Gly Asp Thr Leu 835 840 845	3073
ttc acc acg agc ctg gcc ggc gag gag atc gtc cgg atg cag acc tgg Phe Thr Thr Ser Leu Ala Gly Glu Glu Ile Val Arg Met Gln Thr Trp 850 855 860 865	3121

ggt acg ggc gat atc cgc tac ggg gac tac ctg tcc gga agc ccc tgc Gly Thr Gly Asp Ile Arg Tyr Gly Asp Tyr Leu Ser Gly Ser Pro Cys 870 875 880	3169
acg atg ctc gac att ccg cag ccc ctg atg gag ccg gtg ctg atc aag Thr Met Leu Asp Ile Pro Gln Pro Leu Met Glu Pro Val Leu Ile Lys 885 890 895	3217
aac gcc gcc gaa cgt ggt gcg gtc atc agc ttc aac acc gaa tac ctc Asn Ala Ala Glu Arg Gly Ala Val Ile Ser Phe Asn Thr Glu Tyr Leu 900 905 910	3265
gac cac gcc cag gac gag gac ggg gtg acc gtc cgg ttc cgc gac gtc Asp His Ala Gln Asp Glu Asp Gly Val Thr Val Arg Phe Arg Asp Val 915 920 925	3313
cgc tcg ggc acc gtg ttc acc cag cga gcc cgc ttc ctg ctc ggt ttc Arg Ser Gly Thr Val Phe Thr Gln Arg Ala Arg Phe Leu Leu Gly Phe 930 935 940 945	3361
gac ggc gca cga tcg aag atc gcc gaa cag atc ggg ctt ccg ttc gaa Asp Gly Ala Arg Ser Lys Ile Ala Glu Gln Ile Gly Leu Pro Phe Glu 950 955 960	3409
ggt gaa ctc gcc cgc gcc ggt acc gcg tac atc ctg ttc aac gcg gac Gly Glu Leu Ala Arg Ala Gly Thr Ala Tyr Ile Leu Phe Asn Ala Asp 965 970 975	3457
ctg agc aaa tat gtc gct cat cgg ccg agc atc ttg cac tgg atc gtc Leu Ser Lys Tyr Val Ala His Arg Pro Ser Ile Leu His Trp Ile Val 980 985 990	3505
aac tcg aag gcc ggt ttc ggt gag atc ggc atg ggt ctg ctg cgc gcg Asn Ser Lys Ala Gly Phe Gly Glu Ile Gly Met Gly Leu Leu Arg Ala 995 1000 1005	3553
atc cga ccg tgg gac cag tgg atc gcc ggc tgg ggc ttc gac atg Ile Arg Pro Trp Asp Gln Trp Ile Ala Gly Trp Gly Phe Asp Met 1010 1015 1020	3598
gcg aac ggc gag ccg gat gtc tcc gac gac gtt gtc ctc gaa cag Ala Asn Gly Glu Pro Asp Val Ser Asp Asp Val Val Leu Glu Gln 1025 1030 1035	3643
atc cgg acc ctc gtc ggc gac ccg cac ctg gac gtc gag atc gtg Ile Arg Thr Leu Val Gly Asp Pro His Leu Asp Val Glu Ile Val 1040 1045 1050	3688
tcg agg tcc ttc tgg tac gtc aac cgg cag tgg gct gag cac tac Ser Arg Ser Phe Trp Tyr Val Asn Arg Gln Trp Ala Glu His Tyr 1055 1060 1065	3733
cag tcc ggt cga gtg ttc tgc ggc ggc gac gcg gtg cac ccg cat Gln Ser Gly Arg Val Phe Cys Gly Gly Asp Ala Val His Arg His 1070 1075 1080	3778

ccg Pro 1085	ccg Pro	agc Ser	agc Ser	ggg Gly	ctg Leu 1090	ggc Gly	tcg Ser	aac Asn	acg Thr	tcc Ser 1095	atg Met	cag Gln	gac Asp	gcg Ala	3823
ttc Phe 1100	aac Asn	ctg Leu	gca Ala	tgg Trp	aag Lys 1105	atc Ile	gcg Ala	ttc Phe	gtc Val	gtg Val 1110	aag Lys	ggg Gly	tat Tyr	gca Ala	3868
gga Gly 1115	ccg Pro	ggt Gly	ctg Leu	ctc Leu	gag Glu 1120	tcc Ser	tac Tyr	tct Ser	cct Pro	gag Glu 1125	cgt Arg	gtt Val	ccg Pro	gtc Val	3913
ggc Gly 1130	aaa Lys	cag Gln	atc Ile	gtc Val	gct Ala 1135	cgc Arg	gcc Ala	aac Asn	cag Gln	tcc Ser 1140	cgc Arg	aag Lys	gac Asp	tac Tyr	3958
gcc Ala 1145	ggg Gly	ctg Leu	cgc Arg	gaa Glu	tgg Trp 1150	ttc Phe	gat Asp	cac His	gag Glu	agc Ser 1155	gac Asp	gac Asp	ccg Pro	gtc Val	4003
gcc Ala 1160	gcc Ala	ggc Gly	ctg Leu	gca Ala	aag Lys 1165	ttg Leu	aag Lys	gaa Glu	ccc Pro	tcg Ser 1170	tcc Ser	gaa Glu	ggt Gly	gtt Val	4048
gct Ala 1175	ctg Leu	cgt Arg	gag Glu	cgg Arg	ctg Leu 1180	tac Tyr	gag Glu	gcg Ala	ctg Leu	gag Glu 1185	gtg Val	aag Lys	aac Asn	gcc Ala	4093
gaa Glu 1190	ttc Phe	aac Asn	gcc Ala	cag Gln	ggc Gly 1195	gtc Val	gaa Glu	ctc Leu	aac Asn	cag Gln 1200	cgc Arg	tac Tyr	acc Thr	tcg Ser	4138
tcc Ser 1205	gcg Ala	gtc Val	gtt Val	ccc Pro	gac Asp 1210	ccc Pro	gag Glu	gcg Ala	ggc Gly	gag Glu 1215	gaa Glu	gtg Val	tgg Trp	gtg Val	4183
cgc Arg 1220	gat Asp	cgt Arg	gag Glu	ctg Leu	tac Tyr 1225	ctg Leu	cag Gln	gcc Ala	acc Thr	acc Thr 1230	cgg Arg	ccg Pro	ggc Gly	gcg Ala	4228
aag Lys 1235	ctg Leu	ccg Pro	cat His	gcg Ala	tgg Trp 1240	ctg Leu	gtc Val	ggc Gly	gcc Ala	gac Asp 1245	gga Gly	acc Thr	cgc Arg	atc Ile	4273
tcc Ser 1250	acc Thr	ctc Leu	gac Asp	gtc Val	acc Thr 1255	ggc Gly	aag Lys	gga Gly	atg Met	atg Met 1260	acc Thr	ctg Leu	ctg Leu	acc Thr	4318
gga Gly 1265	ctc Leu	ggc Gly	ggc Gly	cag Gln	gca Ala 1270	tgg Trp	aag Lys	cgt Arg	gcc Ala	gcc Ala 1275	gcc Ala	aaa Lys	ctc Leu	gac Asp	4363
ctg Leu 1280	ccg Pro	ttc Phe	ctg Leu	cgg Arg	acc Thr 1285	gtc Val	gtt Val	gtc Val	ggc Gly	gaa Glu 1290	ccc Pro	ggc Gly	acc Thr	atc Ile	4408

ccccggcgccg accgggccgga tctcacttac ccgacctatt gcgctctcgt ccggaccccc	5680
ggagagaaaag cgccgaagca gcagcaagga gaccgccgcg atg cct gta gcg ctg	5735
Met Pro Val Ala Leu	1400
tgc gcg atg tcg cac tcc ccc ctg atg gga cgc aac gac ccc gaa	5780
Cys Ala Met Ser His Ser Pro Leu Met Gly Arg Asn Asp Pro Glu	1405 1410 1415
cag gaa gtc atc gac gcc gtc gac gcc gca ttc gac cac gcg cgc	5825
Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe Asp His Ala Arg	1420 1425 1430
cgg ttc gtc gcc gac ttc gcc ccc gat ctc atc gtc atc ttc gcc	5870
Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val Ile Phe Ala	1435 1440 1445
ccc gac cac tac aac ggc gtc ttc tac gac ctg ctg ccg ccg ttc	5915
Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro Pro Phe	1450 1455 1460
tgt atc ggt gcc gcc gcg cag tcc gtc ggc gac tac ggc acc gaa	5960
Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr Glu	1465 1470 1475
gcc ggc cct ctc gac gtc gac cgt gac gcc gcc tac gca gtc gcc	6005
Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala	1480 1485 1490
cgc gac gtc ctc gac agc ggc atc gac gtc gca ttc tcc gaa cgc	6050
Arg Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg	1495 1500 1505
atg cac gtc gac cac gga ttc gcc caa gca ctc caa ttg ctg gtc	6095
Met His Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val	1510 1515 1520
gga tcg atc acc gcc gtg ccg acc gtg ccg atc ttc atc aat tcg	6140
Gly Ser Ile Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser	1525 1530 1535
gtc gcc gaa ccg ctc ggc ccg gtc agc cgg gta cgg ctg ctc ggc	6185
Val Ala Glu Pro Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly	1540 1545 1550
gag gcg gtc ggg cgg gcc gct gcc aag ctg gac aag cgt gtg ctg	6230
Glu Ala Val Gly Arg Ala Ala Ala Lys Leu Asp Lys Arg Val Leu	1555 1560 1565
ttc gtc gga tcc ggc ggc ctg tcc cac gac ccg ccg gtc ccg cag	6275
Phe Val Gly Ser Gly Gly Leu Ser His Asp Pro Pro Val Pro Gln	1570 1575 1580
ttc gcc acc gcg cca gag gaa gtg cgc gag cgg ttg atc gac ggc	6320
Phe Ala Thr Ala Pro Glu Glu Val Arg Glu Arg Leu Ile Asp Gly	1585 1590 1595

cgc aat ccc	agt gcc gcc gaa cgt	gat gcc cgc gaa cag	cgc gtc	6365		
Arg Asn Pro	Ser Ala Ala Glu Arg	Asp Ala Arg Glu Gln	Arg Val			
1600	1605	1610				
atc acc gcc	ggg cgg gac ttc gcc	gcc ggc acc gcc gcc	atc cag	6410		
Ile Thr Ala	Gly Arg Asp Phe Ala	Ala Gly Thr Ala Ala	Ile Gln			
1615	1620	1625				
cca ctg aac	ccc gaa tgg gac cgg	cac ctg ctc gac gtc	ctc gcc	6455		
Pro Leu Asn	Pro Glu Trp Asp Arg	His Leu Leu Asp Val	Leu Ala			
1630	1635	1640				
tcc ggc gac	ctc gag cag atc gac	gcg tgg acc aac gac	tgg ttc	6500		
Ser Gly Asp	Leu Glu Gln Ile Asp	Ala Trp Thr Asn Asp	Trp Phe			
1645	1650	1655				
gtc gaa cag	gcc gga cac tcc tcc	cac gaa gtg cgc acc	tgg atc	6545		
Val Glu Gln	Ala Gly His Ser Ser	His Glu Val Arg Thr	Trp Ile			
1660	1665	1670				
gcc gcg tac	gcg gca atg agc gcc	gcc ggg aag tac cgc	gtc acc	6590		
Ala Ala Tyr	Ala Ala Met Ser Ala	Ala Gly Lys Tyr Arg	Val Thr			
1675	1680	1685				
tcg acc ttc	tac cgc gaa atc cac	gag tgg ata gca gga	ttc ggg	6635		
Ser Thr Phe	Tyr Arg Glu Ile His	Glu Trp Ile Ala Gly	Phe Gly			
1690	1695	1700				
att act acc	gcc gtc gcc gtc gac	gaa tag accccgccgc	tcccgccccg	6685		
Ile Thr Thr	Ala Val Ala Val Asp	Glu				
1705	1710					
cagtcccaac	gaaggggtggc	cccggatgac	ctccgtccgc	cctgtgctcgc	cgtcggtgaa	6745
cgcgggctgg	tcgggtgggca	ggaagacctc	atcgccgaca	tcgccctcga	cctcgcagct	6805
cgtcagtagg	aatgcgcacg	ggccgacgag	tcgcgctggt	caccggggcc	agccgcggca	6865
tcggggcggc	catcgcagat	gcggtggccg	cctccggtgc	cgccgtaatc	gtccactacg	6925
gatccgatcg	gacggccgcc	gctgcggtgt	cgacggcatc	acggctgccg	ggggcctcgc	6985
ggctgcggtc	caggccgacc	tgtcccgacc	cgaggggcct	gaagagctga	tgcgggagtt	7045
cgactccgcg	ctcgacggtc	tcgggctcga	ccgagggctc	gacatcctcg	tcaacaacgc	7105
cggaatcagt	cggcgcggag	cgctcgagcg	cgctactgtc	gaggatttcg	accgtctggt	7165
cgactcaac	cagcgcgccc	cgttcttcgt	gactcggcat	gccctgcccc	ggatgcacga	7225
cggcggctgc	atcgtaaca	tttctccgg	atccgcccgc	tacgccagac	ccgacgtcat	7285
cagctacgcc	atgaccaagg	gggcgatcga	ggtgctcacc	cgcgccctcg	ccgtagacgt	7345
cggcgaacga	ggcatcaccg	ccaacgccgt	ggcgccggcc	gcgctcgata	ccgacatgaa	7405
cgcgcactgg	cttcgcggtg	acgaccatgc	ccgcaccacc	gccgcgtcca	ccactgcact	7465

gcgaaaactc gccaccgcgg aggcacatcgc cgcgatcgtg gccttcctcg tcagcgccgc 7525
 cgccggtgcg atcaccgggc aggtcatcga cgccaccaac ggcaaccggc tctaaccaga 7585
 acttaccggg tccc 7599

<210> 2
 <211> 246
 <212> PRT
 <213> Rhodococcus sp.

<400> 2
 Met Thr Thr Thr Asp Thr Gly Pro Lys Pro Gly Ser Glu Ala Ala Ala
 1 5 10 15
 Leu Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala Leu
 20 25 30
 Tyr Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala Gly
 35 40 45
 Glu Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser Lys
 50 55 60
 Gln Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu Val
 65 70 75 80
 His Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro Arg
 85 90 95
 Glu Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr Ile
 100 105 110
 Ala Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu Leu
 115 120 125
 Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro
 130 135 140
 Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala
 145 150 155 160
 Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln
 165 170 175
 Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr
 180 185 190
 Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu
 195 200 205
 Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala
 210 215 220
 Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser
 225 230 235 240

Asn Ala Gln Leu Pro Ser
245

<210> 3

<211> 514

<212> PRT

<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser Pro
1 5 10 15

Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu Arg
20 25 30

Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val Ser
35 40 45

Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala Met
50 55 60

Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile Tyr
65 70 75 80

Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp Val
85 90 95

Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val Gly
100 105 110

Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly Asp
115 120 125

Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met Gly
130 135 140

Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile Gly
145 150 155 160

Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly Phe
165 170 175

Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu His
180 185 190

Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met Gly
195 200 205

Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val Ser
210 215 220

Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro Phe
225 230 235 240

Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu Ser
245 250 255

Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala Val
 260 265 270
 Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu Ile
 275 280 285
 Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr Ile
 290 295 300
 Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile Ser
 305 310 315 320
 Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala Val
 325 330 335
 Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg Lys
 340 345 350
 Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala Pro
 355 360 365
 Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala Ala
 370 375 380
 Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val Thr
 385 390 395 400
 Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser Gly
 405 410 415
 Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe Ala
 420 425 430
 Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn Ser
 435 440 445
 Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser Val
 450 455 460
 Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln Leu
 465 470 475 480
 Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu Thr
 485 490 495
 Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val Leu
 500 505 510

Asp Lys

<210> 4

<211> 637

<212> PRT

<213> Rhodococcus sp.

<400> 4

Val	Met	Thr	Asp	Met	Ser	Asp	His	Asp	Arg	Thr	Ser	Tyr	Asp	Thr	Asp
1				5					10					15	
Val	Val	Ile	Val	Gly	Leu	Gly	Pro	Ala	Gly	Gly	Thr	Ala	Ala	Leu	Ala
			20					25						30	
Leu	Ala	Ser	Tyr	Gly	Ile	Arg	Val	His	Ala	Val	Ser	Met	Phe	Pro	Trp
		35					40					45			
Val	Ala	Asn	Ser	Pro	Arg	Ala	His	Ile	Thr	Asn	Gln	Arg	Ala	Val	Glu
	50					55					60				
Val	Leu	Arg	Asp	Leu	Gly	Val	Glu	Asp	Glu	Ala	Arg	Asn	Tyr	Ala	Thr
65					70					75					80
Pro	Trp	Asp	Gln	Met	Gly	Asp	Thr	Leu	Phe	Thr	Thr	Ser	Leu	Ala	Gly
				85					90					95	
Glu	Glu	Ile	Val	Arg	Met	Gln	Thr	Trp	Gly	Thr	Gly	Asp	Ile	Arg	Tyr
			100					105					110		
Gly	Asp	Tyr	Leu	Ser	Gly	Ser	Pro	Cys	Thr	Met	Leu	Asp	Ile	Pro	Gln
		115					120					125			
Pro	Leu	Met	Glu	Pro	Val	Leu	Ile	Lys	Asn	Ala	Ala	Glu	Arg	Gly	Ala
	130					135					140				
Val	Ile	Ser	Phe	Asn	Thr	Glu	Tyr	Leu	Asp	His	Ala	Gln	Asp	Glu	Asp
145					150					155					160
Gly	Val	Thr	Val	Arg	Phe	Arg	Asp	Val	Arg	Ser	Gly	Thr	Val	Phe	Thr
				165					170					175	
Gln	Arg	Ala	Arg	Phe	Leu	Leu	Gly	Phe	Asp	Gly	Ala	Arg	Ser	Lys	Ile
			180					185					190		
Ala	Glu	Gln	Ile	Gly	Leu	Pro	Phe	Glu	Gly	Glu	Leu	Ala	Arg	Ala	Gly
		195					200					205			
Thr	Ala	Tyr	Ile	Leu	Phe	Asn	Ala	Asp	Leu	Ser	Lys	Tyr	Val	Ala	His
	210					215					220				
Arg	Pro	Ser	Ile	Leu	His	Trp	Ile	Val	Asn	Ser	Lys	Ala	Gly	Phe	Gly
225					230					235					240
Glu	Ile	Gly	Met	Gly	Leu	Leu	Arg	Ala	Ile	Arg	Pro	Trp	Asp	Gln	Trp
				245					250					255	
Ile	Ala	Gly	Trp	Gly	Phe	Asp	Met	Ala	Asn	Gly	Glu	Pro	Asp	Val	Ser
			260					265					270		
Asp	Asp	Val	Val	Leu	Glu	Gln	Ile	Arg	Thr	Leu	Val	Gly	Asp	Pro	His
		275					280					285			
Leu	Asp	Val	Glu	Ile	Val	Ser	Arg	Ser	Phe	Trp	Tyr	Val	Asn	Arg	Gln
	290					295					300				

Trp Ala Glu His Tyr Gln Ser Gly Arg Val Phe Cys Gly Gly Asp Ala
 305 310 315 320
 Val His Arg His Pro Pro Ser Ser Gly Leu Gly Ser Asn Thr Ser Met
 325 330 335
 Gln Asp Ala Phe Asn Leu Ala Trp Lys Ile Ala Phe Val Val Lys Gly
 340 345 350
 Tyr Ala Gly Pro Gly Leu Leu Glu Ser Tyr Ser Pro Glu Arg Val Pro
 355 360 365
 Val Gly Lys Gln Ile Val Ala Arg Ala Asn Gln Ser Arg Lys Asp Tyr
 370 375 380
 Ala Gly Leu Arg Glu Trp Phe Asp His Glu Ser Asp Asp Pro Val Ala
 385 390 395 400
 Ala Gly Leu Ala Lys Leu Lys Glu Pro Ser Ser Glu Gly Val Ala Leu
 405 410 415
 Arg Glu Arg Leu Tyr Glu Ala Leu Glu Val Lys Asn Ala Glu Phe Asn
 420 425 430
 Ala Gln Gly Val Glu Leu Asn Gln Arg Tyr Thr Ser Ser Ala Val Val
 435 440 445
 Pro Asp Pro Glu Ala Gly Glu Glu Val Trp Val Arg Asp Arg Glu Leu
 450 455 460
 Tyr Leu Gln Ala Thr Thr Arg Pro Gly Ala Lys Leu Pro His Ala Trp
 465 470 475 480
 Leu Val Gly Ala Asp Gly Thr Arg Ile Ser Thr Leu Asp Val Thr Gly
 485 490 495
 Lys Gly Met Met Thr Leu Leu Thr Gly Leu Gly Gly Gln Ala Trp Lys
 500 505 510
 Arg Ala Ala Ala Lys Leu Asp Leu Pro Phe Leu Arg Thr Val Val Val
 515 520 525
 Gly Glu Pro Gly Thr Ile Asp Pro Tyr Gly Tyr Trp Arg Arg Val Arg
 530 535 540
 Asp Ile Asp Glu Ala Gly Ala Leu Leu Val Arg Pro Asp Gly Tyr Val
 545 550 555 560
 Ala Trp Arg His Ser Ala Pro Val Trp Asp Asp Thr Glu Ala Leu Thr
 565 570 575
 Ser Leu Glu Asn Ala Leu Thr Ala Val Leu Asp His Ser Ala Ser Asp
 580 585 590
 Asn Gly Asn Pro Ser Gly Thr Asn Glu Pro Gln Tyr Ser Thr Arg Ala
 595 600 605

Val Pro Ile Val Val Pro His Val Thr Ala Glu Asp Ala Ala Pro Ala
610 615 620

Ser Ala Thr Arg Thr Thr Thr Val Glu Gly Glu Asn Arg
625 630 635

<210> 5

<211> 314

<212> PRT

<213> Rhodococcus sp.

<400> 5

Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly Arg
1 5 10 15

Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe Asp
20 25 30

His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val Ile
35 40 45

Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro Pro
50 55 60

Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr Glu
65 70 75 80

Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala Arg
85 90 95

Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met His
100 105 110

Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser Ile
115 120 125

Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu Pro
130 135 140

Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly Arg
145 150 155 160

Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly Gly
165 170 175

Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu Glu
180 185 190

Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu Arg
195 200 205

Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala Ala
210 215 220

Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His Leu
225 230 235 240


```
<210> 6
<211> 870
<212> DNA
<213> Rhodococcus sp.
```

```
<220>  
<221> CDS  
<222> (1) .. (867)
```

<400> 6																
atg	acc	cgt	cct	tac	acc	agc	gtc	tgg	gac	gac	ctg	aac	cag	gtc	gag	48
Met	Thr	Arg	Pro	Tyr	Thr	Ser	Val	Trp	Asp	Asp	Leu	Asn	Gln	Val	Glu	
1				5				10				15				
ttc	agc	cag	gga	ttc	atc	cag	gcc	ggc	ccc	tac	cgg	acc	cga	tac	ctg	96
Phe	Ser	Gln	Gly	Phe	Ile	Gln	Ala	Gly	Pro	Tyr	Arg	Thr	Arg	Tyr	Leu	
20				25				30								
cac	gcc	ggc	gat	tcg	tcc	aag	ccc	acg	ctg	atc	ctg	ctg	cac	ggc	atc	144
His	Ala	Gly	Asp	Ser	Ser	Lys	Pro	Thr	Leu	Ile	Leu	Leu	His	Gly	Ile	
35				40				45								
acc	ggc	cac	gcc	gag	gcg	tac	gtg	cgc	aat	ctg	cgc	tcg	cat	tcc	gag	192
Thr	Gly	His	Ala	Glu	Ala	Tyr	Val	Arg	Asn	Leu	Arg	Ser	His	Ser	Glu	
50				55				60								
cac	ttc	aac	gtc	tgg	gca	atc	gac	ttc	atc	ggc	cac	ggc	tat	tcg	acc	240
His	Phe	Asn	Val	Trp	Ala	Ile	Asp	Phe	Ile	Gly	His	Gly	Tyr	Ser	Thr	
65				70				75				80				
aag	ccc	gac	cac	ccg	ctc	gag	atc	aag	cac	tac	atc	gac	cag	gtg	ctg	288
Lys	Pro	Asp	His	Pro	Leu	Glu	Ile	Lys	His	Tyr	Ile	Asp	Gln	Val	Leu	
85				90				95								
cag	ttg	ctg	gac	gcc	atc	ggc	gtc	gag	aag	gcc	tcg	ttt	tcc	ggg	gag	336
Gln	Leu	Leu	Asp	Ala	Ile	Gly	Val	Glu	Lys	Ala	Ser	Phe	Ser	Gly	Glu	
100				105				110								

tct ctc ggc ggt tgg gtc acc gcc cag ttc gcg cac gac cat ccc gag	384
Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu	
115 120 125	
aag gtc gac cgg atc gtg ctc aac acc atg ggc ggc acc atg gcc aac	432
Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn	
130 135 140	
cct cag gtg atg gaa cgt ctc tat acc ctg tgc atg gaa gcg gcg aag	480
Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys	
145 150 155 160	
gac ccg agc tgg gaa cgc gtc aaa gca cgc ctc gaa tgg ctc atg gcc	528
Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala	
165 170 175	
gac ccg acc atg gtc acc gac gac ctg atc cgc acc cgc cag gcc atc	576
Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile	
180 185 190	
ttc cag cag ccg gat tgg ctc aag gcc tgc gag atg aac atg gca ctg	624
Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu	
195 200 205	
cag gac ctc gaa acc cgc aag cgg aac atg atc acc gac gcc act ctc	672
Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu	
210 215 220	
aac ggc atc acg gtg ccc gcg atg gtg ctg tgg acc acc aag gac ccc	720
Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro	
225 230 235 240	
tcc ggt ccg gtc gac gaa gcc aag cgc atc gcc tcc cac atc ccg ggc	768
Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly	
245 250 255	
gcc aag ctg gcc atc atg gag aac tgt ggc cac tgg ccc cag tac gag	816
Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu	
260 265 270	
gac ccc gag acc ttc aac aag ctg cat ctg gac ttc ctc ctc ggt cgc	864
Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg	
275 280 285	
agc tga	870
Ser	

<210> 7

<211> 289

<212> PRT

<213> Rhodococcus sp.

<400> 7

Met Thr Arg Pro Tyr Thr Ser Val Trp Asp Asp Leu Asn Gln Val Glu
1 5 10 15

Phe Ser Gln Gly Phe Ile Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu
 20 25 30
 His Ala Gly Asp Ser Ser Lys Pro Thr Leu Ile Leu Leu His Gly Ile
 35 40 45
 Thr Gly His Ala Glu Ala Tyr Val Arg Asn Leu Arg Ser His Ser Glu
 50 55 60
 His Phe Asn Val Trp Ala Ile Asp Phe Ile Gly His Gly Tyr Ser Thr
 65 70 75 80
 Lys Pro Asp His Pro Leu Glu Ile Lys His Tyr Ile Asp Gln Val Leu
 85 90 95
 Gln Leu Leu Asp Ala Ile Gly Val Glu Lys Ala Ser Phe Ser Gly Glu
 100 105 110
 Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu
 115 120 125
 Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn
 130 135 140
 Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys
 145 150 155 160
 Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala
 165 170 175
 Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile
 180 185 190
 Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu
 195 200 205
 Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu
 210 215 220
 Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro
 225 230 235 240
 Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly
 245 250 255
 Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu
 260 265 270
 Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg
 275 280 285

Ser

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig OHPR3

<400> 8
 atcgaattcg gatccatgac caccacc 27

<210> 9
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig OHPR4

<400> 9
 atcgcggccg ctctagacta actgcagggc gccaaagctcg gcag 44

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig C11

<400> 10
 atcgaattcg gatccacgag agag 24

<210> 11
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig C12

<400> 11
 atccggccgc gctctagagt acgcaagct 29

<210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig op1

<400> 12
 atcctcgaga ccccgataacc 20

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig op2

<400> 13
 atcgtcgacc gctaccc 17

<210> 14
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop2

<400> 14
 tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc 50

<210> 15
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop3

<400> 15
 atgctagacg tctagttcag acgctactta tatagaggaa gggctcttgcg 50

<210> 16
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop4

<400> 16
 cgtctagcat tctagttgag gaagttcatt tcatttggag aggac 45

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic olig CaMVopF1

<400> 17

atcgatatct ccactgacgt aag

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic olig CaMVopR1

<400> 18

gatggatccg tcctctccaa atga

24

<210> 19

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Promoter

<400> 19

catgcctgca	ggtcaacatg	gtggagcacg	acactctcgt	ctactccaag	aatatcaaag	60
atacagtctc	agaagaccag	agggctattg	agacttttca	acaaagggta	atatcgggaa	120
acctcctcgg	attccattgc	ccagctatct	gtcacttcat	cgaaaggaca	gtagaaaagg	180
aagatggctt	ctacaaatgc	catcattgcg	ataaaggaaa	ggctatcggt	caagaatgcc	240
tctaccgaca	gtggtcccaa	agatgtaccc	ccaccacga	ggaacatcgt	ggaaaaagaa	300
gacgttccaa	ccacgtcttc	aaagcaagtg	gattgatgtg	atatctccac	tgacgtaagg	360
gatgacgcac	aatcccacta	tccttcgcaa	gacccttcct	ctatataagt	agcgtctgaa	420
ctagacgtct	agcattctag	ttgaggaagt	tcatttcatt	tgagaggac		470